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Kelley Heffner

Johns Hopkins University, kel24@jhu.edu

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ELUCIDATING CELL LINE AND TISSUE DIFFERENCES DERIVED FROM *CRICETULUS GRISEUS* BY TRANSCRIPTOMICS AND PROTEOMICS

Kelley Heffner, Johns Hopkins University USA
KEL24@jhu.edu

Deniz Baycin Hizal, MedImmune USA

Michael Bowen, MedImmune USA

Robert Cole, Johns Hopkins Medical Institute USA

Robert O'Meally, Johns Hopkins Medical Institute USA

Michael Betenbaugh, Johns Hopkins University USA

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Chinese hamster ovary (CHO) cells derived from *Cricetulus griseus* remain the dominant host for recombinant protein production. This project aims to expand our knowledge by conducting transcriptomics and proteomics experiments on CHO cell lines and Chinese hamster tissues in order to obtain a larger set of genetic engineering targets for improving bioprocess development. This study will increase data sets using cell line comparisons and investigate how mRNA and protein levels change from Chinese hamster lineage. Quantitative 'omics data from CHO cell lines and Chinese hamster tissues data was obtained by RNAseq (transcriptome) and labeled tandem mass tag mass spectrometry (proteome). Plots of comparative protein intensity, as measured by normalized spectral abundance factor, of Chinese hamster tissues and CHO cell lines at exponential and stationary phases were created. Data points exhibit varying amounts of scatter indicating differences in protein levels between tissues and cell lines. From the plots, outlier points were identified and functionally analyzed in order to suggest targets of opportunity within important physiological pathways. Overexpression or inhibition of these potential targets may yield bioprocess development improvements.